Amendments to the Claims:

Please amend claim 1. This listing of claims replaces all prior versions, and listings of claims in the application.

Listing of Claims:

1. (Currently Amended) A multiplexed method of detecting a plurality of target polypeptides in a sample composition, the method comprising:

a) contacting the sample composition with genetic packages that each display a polypeptide-binding component under conditions whereby the plurality of target polypeptides in the sample form complexes with displayed polypeptide-binding components specific therefor, wherein:

each genetic package comprises a predetermined marker component that is indicative of the displayed polypeptide-binding component;

the polypeptide-binding component specifically binds to at least one of the target polypeptides, whereby target polypeptides that bind thereto can be identified by virtue of the marker component; and

wherein the genetic packages are selected from the group consisting of a bacteriophage, a virus [[or]] and a bacterium;

b) separating complexes of the plurality of target polypeptides with the displayed polypeptide-binding components on the genetic packages from the sample composition;

c) optionally amplifying the genetic packages that have formed complexes, resulting in amplified genetic packages, or amplifying the marker components in the genetic packages that have formed complexes;

d) identifying marker components in the genetic packages that have formed complexes, thereby detecting the plurality of target polypeptides in the sample, wherein:

identification of a marker component is effected by mass spectrometry; and

identification of a marker component indicates the presence of a target polypeptide in the sample.

2. (Previously Presented) The method of claim 1, wherein the target polypeptides comprise one or more proteins, biotinylated proteins, isolated proteins, recombinant proteins, enzymes, enzyme substrates, cancer proteins, or disease related proteins.

3. (Previously Presented) The method of claim 1, wherein target polypeptides in the sample or genetic packages in the sample are bound to a solid support.

4. (Original) The method of claim 3, wherein the solid support comprises one or more of a microsphere or bead, a surface of a tube or plate or a filter membrane.

5. (Original) The method of claim 3, further comprising washing the solid support after the polypeptide binding component specifically binds at least one of the one or more polypeptides.

6. (Original) The method of claim 1, comprising concurrently detecting at least about 10 to about 109 polypeptides.

7. (Original) The method of claim 6, comprising concurrently detecting at least about 50 to about 10,000 polypeptides.

8. (Original) The method of claim 6, comprising concurrently detecting at least about 3 to about 500 polypeptides.

9. (Original) The method of claim 6, comprising concurrently detecting at least about 3 to about 100 polypeptides.

10. (Original) The method of claim 1, wherein the sample is a tissue sample, a blood sample, a cell lysate or a plurality of cultured cells.

11. (Original) The method of claim 1, wherein the virus comprises a baculovirus.

12. (Previously Presented) The method of claim 1, wherein the bacteriophage comprises T4 phage, M13 phage or lambda phage.

13. (Cancelled)

14. (Previously Presented) The method of claim 1, wherein the plurality of bio-displayed polypeptide binding components comprises about 102 to about 1010 different polypeptide-binding components.

15. (Previously Presented) The method of claim 1, wherein the plurality of bio-displayed polypeptide binding components comprises about 105 to about 1010 different polypeptide-binding components.

16-17. (Cancelled)

18. (Original) The method of claim 1, wherein the polypeptide-binding component comprises one or more of an agent selected from among an antibody, an antibody fragment, a single chain antibody fragment, an enzyme, biotin, avidin, streptavidin, a ligand and a receptor.

19. (Original) The method of claim 18, wherein the antibody, the antibody fragment or the single chain antibody fragment comprises one or more antigen recognition regions.

20. (Cancelled)

21. (Previously Presented) The method of claim 1, wherein mass spectrometry format comprises matrix-assisted laser desorption/ionization (MALDI) time-of-flight (TOF) mass spectrometry.

22. (Original) The method of claim 1, further comprising determining an amount of the marker component.

23. (Original) The method of claim 22, comprising correlating the amount of the marker component to an amount of at least one of the one or more polypeptides in the sample.

24-25. (Cancelled)

26. (Original) The method of claim 1, wherein the genetic package comprises a surface and wherein the marker component comprises a nucleic acid, which nucleic acid encodes a polypeptide, which polypeptide is expressed on the surface of the genetic package.

27. (Previously Presented) The method of claim 1, wherein the predetermined marker component comprises a nucleic acid fragment.

28. (Original) The method of claim 27, wherein amplifying the marker component comprises performing polymerase chain reaction, ligase chain reaction, or Qβ-replicase amplification of the nucleic acid fragment or a detectable portion thereof.

29-48. (Cancelled)

49. (Previously Presented) The method of claim 1, wherein the genetic packages or nucleic acid molecules encoding the predetermined marker components are amplified prior to detection of the markers.

50. (Previously Presented) The method of claim 49, wherein amplifying the genetic packages comprises performing polymerase chain reaction, ligase chain reaction, or Qβ-replicase amplification of the nucleic acid molecule encoding the predetermined marker component or

amplifying or a detectable portion of the nucleic acid molecule encoding the predetermined marker component.

51. (Cancelled)